What is Claimed is:

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1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on at least one copy of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

			HA	PLO:	TYPE	ug :	JMB1	ER ^a			$\mathtt{PS}^\mathtt{b}$		PS .	
10	1	2	3 4	5	6	7	8	9	10	NUI	MBER			TION°
	G		G G	G	G	G	G	G	G		1		3102	
	G		G G	G	G	G	g	G	G		2		3409	
١	A		A A	A	A	A	A^{\setminus}	A	A		3		3438	
,	С		C C	C	С	С	С	\sqrt{C}	С		4		3603	
15	A		A A	Ā	A	Ā	G	ģ	G		5		4054	
	G		G G	G	G	G	G	G)	G		6		4082	
	C		C C	C	Ċ	C	C	C \	\c_		7		1199	
<u> </u>	G		G G	G	G	G	Ā	G	É		8		1235	
	T		T T	T	$\overset{\circ}{\mathrm{T}}$	T	T	C	T		9		1239	
:#20	Ĉ		CC	Ĉ	Ĉ	Ĉ	C	Ċ	c\		10		1248	
47°	C		CC	C	C	C	C	C	C	\	11		1265	
5.3 E 4994	A		G G	G	G	G	G	G	G		12		1482	
And the control of th	A		A A	A	G	G	G	A	A	1	13		1499	
	C		CC	T	C	C	C	C	C	/	13		1508	
# 25	C		C T	C	C	C	C	C	C		15		1509	
<u></u> 25	C		T C	C	C	T	T	T	C		76		1552	
144	G		G G	G	G	G	G	G.	G		1 1		1593	
	G		G G	G	G	G	G	G	G		18		1616	
energ page	G	G	o o	G	G	G	G	G	G		TO /		1010	, ,
1130			IJΛ	DT.O	rype	' NIT	JMBI	грa			,	\	PS ^b	PS
	11	12		14	15		16	17	18	1	9 20	ATTI	MBER	POSITION ^c
	G	G G	G	G	G		G G	G ,	G	G	9 20 G	1,01	1	3102
	G	G	G	G	G		G G	G	T	T	T	1	2	3409
	A	A	A	A	G		G	G	Ā	A)	A	1	\ 3	3438
35	C	C	C	C	C		C	C	C	C	C			3603
55	G	G	G	G	A		A.	A	A	A	A		\4 5\	4054
	G	G	G	G	G		G.	G	A	G	G		6	4082
	C	C	C	T	C		C	T	C	C	C		7	11998
	G	G	G	Ğ	G		G G	G	G	G	G		8	12356
40	T	T	T	T	T		ľ	T	T	T	T		9	12397
10	C	Ĉ	Ċ	Ċ	C		C	Ċ	Ċ	C	Ċ		10	12489
	C	C	T	C	C		C	C	T	C	C		11	12653
	G	G	G	G	G		G	G	G	G	G		12	14824
	A	G	A	G	A		A A	A	A	A	G		13	14990
45	C	C	C	C	C		C	C	C	C	C		14	15089
73	C	C	C	C	C		C	C	C	C	C		15	15093
	T	T	T	T	C		ľ	C	T	T	T		16	15529
	G	G	G	G	G		ц G	G	G	A	G		17	15932
	G	G	G	G	G		g G	G	G	A G	G		18	16165
50	G	G	G	G	G		J	G	G	G	G		ΤO	10100
50														1

			НΖ	PLOT	YPE	NUME	FPa		PS ^b	PS
	21	22	23	• 24	25	26	27		NUMBER	POSITION°
	G	G	G	\sqrt{G}	G	G	T		1	3102
	T	T	T	7	T	T	G .		2	3409
5	Ā	A	Ā	Ā	Ā	Ğ	G		3	3438.
3	C	C	C	C /	G	C	C		4	3603
	A	A	A	G	\sqrt{A}	A	A		5	4054
	G	G	G	G	Ž,	G	G		6	4082
	C	C	C	C	c/	. C	C		7	11998
10	Ğ	G	G	G	G	G	G		8	12356
10	T	T	T	T	T	A.	T		9	12397
	Ĉ	Ċ	T	Ĉ	Ċ	cl	Ĉ		10	12489
	T	$\overset{\smile}{ ext{T}}$	T	T	T	c\	Č		11	12653
	G	G	Ğ	Ğ	Ġ	G	\ Ğ		12	14824
15	A	A	A	A	A	A	XI		13	14990
10	C	C	C	C	C	C	Ş		14	15089
	C	C	C	C	Ċ	C	c\		15	15093
	C	T	T	T	T	C	T		16	15529
	G	Ğ	G	Ğ	G	G	Ğ,	\	17	15932
-20	G	G	G	G	G	G	A	1	18	16165
	G	G	G	G	J	J	Λ	\	10	10100

^aAlleles for haplotypes are presented 5 to 3' in each column

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on both copies of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

^bPS = polymorphic site;

^cPosition of PS within SEQ ID NO:1.

-	5	HAPLOT 12/12 G/G G/G A/A C/C G/G G/G	TYPE PA 22/22 G/G T/T A/A C/C A/A G/G	IR ^a 2	22/20 G/G T/T A/A C/C A/A G/G	12/10 G/G G/G A/A C/C G/G G/G	2/1 G/G G/G A/A C/C A/A G/G	22/23 G/G T/T A/A C/C A/A G/G	2/11 G/G G/G A/A C/C A/G G/G	PS ^b NUMBER 1 2 3 4 5	PS POSITION ^c 3102 3409 3438 3603 4054 4082
	10	C/C G/G T/T C/C	C/C G/G T/T C/C	C/C G/G T/T C/C	C/C G/G T/T C/C	C/C G/G T/T C/C	C/C G/G T/T C/C	C/C G/G T/T C/T	C/C G/G T/T C/C	7 8 9 10	11998 12356 12397 12489
C. B	15	C/C G/G	T/T G/G	C/C G/G	T/C G/G	¢∕c GXG	C/C G/A	T/T G/G	C/C G/G	11 12	12653 14824
920		G/G C/C	A/A C/C	A/A C/C	A/G C/C	G/A C/C	A/A C/C	A/A C/C	A/A C/C	13 14	14990 15089
CON		C/C	C/C	C/C	C/C	c/c \	C/C	C/C	C/C	15	15093
	it.	T/T	T/T	C/C	T/T	T/C \	C/C	T/T	C/T	16	15529
(00)	20	G/G	G/G	G/G	G/G	G/G	\ G/G	G/G	G/G	17	15932 16165
	Sec.	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	10103
	. 275						1			L.	
	Tribert 1880	HAPLO	TYPE PA	I R ^a			\			PS ^b	PS
			TYPE PA	IR ^a 12/1	5 22/8	2/9	3/21	2/15	12/17	PS ⁵ NUMBER	POSITIONC
		HAPLO' 2/19 G/G	TYPE PA 3/14 G/G	IR ^a 12/1 G/G	5 22/8 G/G	2/9 G/G	G/G∖	G/G	G/G	NUMBER 1	POSITION ^c 3102
		2/19	3/14	12/1			G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITION ^c 3102 3409
	And the state of t	2/19 G/G	3/14 G/G G/G A/A	12/1 G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G ∖A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
		2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/1 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
		2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/1 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
		2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/1 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
		2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/1 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/1 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/1 G/G G/G A/G C/C G/A G/G C/C G/C G/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/1 G/G G/G A/G C/C G/A G/G C/C G/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/C C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G G/A	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G T/T C/C G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	und den den den den den den den den den d	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/C C/C G/G A/G C/C	G/G G/G A/A C/C A/G G/C C/C G/C C/C C/C C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/G G/T C/C G/A C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
	The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/T G/A	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/C C/C T/T G/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A C/C C/C G/G G/A	G/G T/G A/A C/C A/G G/C T/C T/C G/G C/C T/T G/G	G/G G/G A/A C/C A/G G/C C/C G/A C/C C/C G/A C/C C/T G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C T/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C G/G	G/G G/G A/G C/A G/G G/G T/T C/C G/A C/C G/A C/C G/G G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932
	The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/C C/C T/T	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C T/C	G/G T/G A/A C/C A/G C/A T/C T/C G/G C/C T/T	G/G G/G A/A C/C A/G G/C C/C G/C C/C C/C C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/G G/T C/C G/A C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

2/21 22/3 22/25 12/25 12/24 12/13 3/16 22/16 NUMBER POSITION	I		HAPLOT	YDE	IRª						PS^b	PS
G/G G/G G/G G/G G/G G/G G/G G/G G/G 1 3102 G/T T/G T/T G/T G/T G/T G/G G/G T/G 2 3409 5 A/A A/A A/A A/A A/A A/A A/A A/A A/G A/G						12/25	12/24	12/13	3/16	22/16		
S												
5 A/A A/A A/A A/A A/A A/A A/A A/G A/G A/G												
C/C C/C C/G C/G C/C C/C C/C C/C 4 3603 A/A A/A A/A A/A G/A G/G G/G A/A A/A 5 4054 G/G G/G G/G G/G G/G G/G G/G G/G G/G G/		5			1							
A/A A/A A/A G/A G/A G/G G/G A/A A/A 5 4054 G/G G/G G/G G/G G/G G/G G/G G/G G/G G/		-			1							
G/G G/G G/G G/G G/G G/G G/G G/G G/G G/					Y		-					
C/C C/C C/C C/C C/C C/C C/C C/C C/C 7 11998 10	ļ				.7							
10	İ				١.							
T/T		10									8	
C/C					•					T/T	9	
C/T	l			C/C	C/C	¢\c	C/C	C/C	C/C	C/C	10	12489
SWB 15						c∕\T	C/T	C/T	C/C	T/C	11	12653
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONC G/T G/G G/G G/G G/G G/G G/G G/G T/G T/T 2 3409 A/G A/A A/G A/A A/A A/A A/A A/A A/A A/A	1 2		G/G	G/G	G/G	G∕G	G/G	G/G	G/G	G/G	12	14824
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONC G/T G/G G/G G/G G/G G/G G/G G/G T/G T/T 2 3409 A/G A/A A/G A/A A/A A/A A/A A/A A/A A/A	1349	15	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONS			C/C	C/C	C/C	c/c\	C/C	C/C	C/C	C/G	14	15089
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONC G/T G/G G/G G/G G/G G/G G/G G/G T/G T/T 2 3409 A/G A/A A/G A/A A/A A/A A/A A/A A/A A/A	101		C/C	C/C	C/C	c/c \	C/C	C/C	C/C	C/C	15	15093
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONC G/T G/G G/G G/G G/G G/G G/G G/G T/G T/T 2 3409 A/G A/A A/G A/A A/A A/A A/A A/A A/A A/A	I FI	٠		T/T	T/T		T/T					
HAPLOTYPE PAIRa 3/27 22/10 2/16 2/26 22/11 12/7 22/2 22/18 NUMBER POSITIONC G/T G/G G/G G/G G/G G/G G/G G/G T/G T/T 2 3409 A/G A/A A/G A/A A/A A/A A/A A/A A/A A/A	1207	*					ν.					
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A/A A/G A/A A/A A/G G/A A/A A/A 5 4054 G/G G/G G/G G/G G/G G/G G/G G/A 6 4082 C/C C/C C/C C/C C/C C/C C/C C/C 7 11998 G/G G/G G/G G/G G/G G/G G/G G/G B 12356 T/T T/T T/T T/T T/T T/T T/T T/T T/T T/			3/27	22/10	2/16						NUMBER	POSITION°
A/A A/G A/A A/A A/G G/A A/A A/A 5 4054 G/G G/G G/G G/G G/G G/G G/G G/A 6 4082 C/C C/C C/C C/C C/C C/C C/C C/C 7 11998 G/G G/G G/G G/G G/G G/G G/G G/G B 12356 T/T T/T T/T T/T T/T T/T T/T T/T T/T T/			3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
A/A A/G A/A A/A A/G G/A A/A A/A 5 4054 G/G G/G G/G G/G G/G G/G G/G G/A 6 4082 C/C C/C C/C C/C C/C C/C C/C C/C 7 11998 G/G G/G G/G G/G G/G G/G G/G G/G B 12356 T/T T/T T/T T/T T/T T/T T/T T/T T/T T/			3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION° 3102 3409
G/G G/G G/G G/G G/G G/G G/G G/A 6 4082 C/C C/C C/C C/C C/C C/C C/C C/C 7 11998 G/G G/G G/G G/G G/G G/G G/G G/G G/G 8 12356 T/T T/T T/T T/T T/T T/T T/T T/T T/T T/			3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G AXA	G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
30		The state of the s	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G AXA C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION° 3102 3409 3438 3603
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B5 G/G G/G G/G G/G G/G G/G G/G 12 14824 A/A A/A A/A A/A A/A G/G A/A A/A 13 14990 C/C C/C C/C C/C C/C C/C C/C 14 15089 C/C C/C C/C C/C C/C C/C C/C 15 15093		Ų.	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G AXA C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054 4082
B5 G/G G/G G/G G/G G/G G/G G/G 12 14824 A/A A/A A/A A/A A/A G/G A/A A/A 13 14990 C/C C/C C/C C/C C/C C/C C/C 14 15089 C/C C/C C/C C/C C/C C/C C/C 15 15093		Ų.	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G AXA C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION° 3102 3409 3438 3603 4054 4082 11998
B5 G/G G/G G/G G/G G/G G/G G/G 12 14824 A/A A/A A/A A/A A/A G/G A/A A/A 13 14990 C/C C/C C/C C/C C/C C/C C/C 14 15089 C/C C/C C/C C/C C/C C/C C/C 15 15093		Ų.	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G AXA C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356
A/A A/A A/A A/A G/G A/A A/A 13 14990 C/C C/C C/C C/C C/C C/C C/C 14 15089 C/C C/C C/C C/C C/C C/C C/C 15 15093		Ų.	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/C C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397
C/C C/C C/C C/C C/C C/C C/C 14 15089 C/C C/C C/C C/C C/C C/C 15 15093			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G AXA C/C G/A G/C C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
C/C C/C C/C C/C C/C C/C \ C/C 15 15093			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/A C/A G/C G/G T/T C/C G/G G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/C C/C A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/GA C/A C/A C/C G/G T/T C/C G/G C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
l			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/C G/G T/C C/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C C/C	G/G G/GAACAACAACAAACAAAAAAAAAAAAAAAAAAAA	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/G T/T C/T G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C G/C A/A C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C T/T	G/G G/G A/A C/A G/G C/C G/G C/C G/C C/C T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/A G/C G/G T/T G/A C/C T/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
G/A G/G G/G G/G G/G G/G 18 16165			3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C G/G A/A C/C C/C G/G	22/10 G/G T/G A/A C/C A/G G/C G/C T/T C/C G/A C/C T/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C G/G	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/A C/C T/T G/G	G/G G/G A/A C/A C/A C/C G/C C/C G/C C/C G/C C/T G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/C G/G A/A C/C C/C T/C G/G	G/G T/A C/A C/A C/G/T C/T G/A C/T G/A C/T G/A C/T G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932

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HAPLOT	YPE PA	IR ^a				PS ^b	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITIONC
G/G	G/G \	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	\ G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	cXc	C/C	C/C	C/C	4	3603
A/G	G/A	G/À	G/A	G/A	A/A	5	4054
G/G	G/G	G/G\	G/G	G/G	G/G	6	4082
C/C	C/C	C/C `	\C/C	T/C	C/C	7	11998
G/G	G/G	G/G	Ġ√G	G/G	G/G	8	12356
T/T	T/T	T/T	т Хт	T/T	T/T	9	12397
C/C	C/C	C/C	c/ <i>q</i>	C/C	C/C	10	12489
T/C	C/C	C/C	c/c\	C/C	C/C	11	12653
G/G	G/G	G/G	G/G \	G/G	G/G	12	14824
A/G	G/A	G/A	G/A \	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	℃ /C	C/C	14	15089
C/C	C/C	C/C	C/C	cXc	C/T	15	15093
T/T	T/C	T/T	T/C	$\mathbb{Z} \setminus \mathbb{T}$	T/C	16	15529
G/G	G/G	G/G	G/G	G/G\	G/G	17	15932
G/G	G/G	G/G	G/G	G/G \	G/G	18	16165
				1			

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column; ^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1.

- 3. A method for genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, comprising determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the one or more PS have the position and alternative alleles shown in SEQ ID NO:1.
- 4. The method of claim 3, wherein the determining step comprises:
 - (a) isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF1A gene, or a fragment thereof, that are present in the individual;
 - (b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;
 - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.

- 5. The method of claim 3, which comprises determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at each of PS1-PS18.
- 6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual which comprises determining, for one copy of the TNFRSF1A gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 7. The method of claim 6, further comprising determining the identity of the nucleotide at one or more polymorphic sites selected from the group consisting of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, which has the location and alternative alleles shown in SEQ ID NO: 1.
- 8. The method of claim 6, wherein the determining step comprises:
 - a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF1A gene, or a fragment thereof, that is present in the individual;
 - (b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in the target region;
 - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
- 9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual comprising:
 - (a) identifying a TNFRSF1A genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;
 - (b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and
 - (c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

	HAPLOT	TYPE PA	.IRª						PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITIONC
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
15	G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G .	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
20	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
	C/C	T/T	C/C	T/C	C/C	C/C	\mathtt{T}/\mathtt{T}	C/C	11	12653
25	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
<u>30</u>	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
lad . M	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
73.2										
489										
		YPE PA							PS ^b	PS
	2/19	3/14	12/15	5 22/8	2/9	3/21	2/15	12/17	NUMBER	POSITIONC
	2/19 G/G	3/14 G/G	12/15 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION ^c 3102
	2/19 G/G G/T	3/14 G/G G/G	12/15 G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITION° 3102 3409
Sand Lines	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/15 G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
The same of the sa	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/15 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/15 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/15 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/15 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
Confirmation of Confirmation	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
Confirmation of Confirmation	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/C C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/C C/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T G/C C/C G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C	12/15 G/G G/G A/G C/C G/A G/C C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G C/C	G/G G/G A/A C/C A/G G/C C/C G/G T/C C/C G/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
Sand small to the Market court court of the Market court of the Ma	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/C C/C C/C	12/15 G/G G/G A/G C/C G/A G/C C/C C/C C/C C/C C/C C/C	G/G T/A C/C A/G G/C C/A T/T C/C G/G A/C C/C C/C	G/G G/G A/A C/C A/G G/C C/C C/C G/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G T/T C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
The state of the s	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/G T/T C/C G/G A/C C/C T/T	12/15 G/G G/G A/C G/A G/C G/G T/T C/C G/A C/C T/C	G/G T/A C/C A/G G/C C/A T/C C/C G/G C/C T/T C/C T/T	G/G G/G A/A C/C A/G G/C C/C G/A C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/C C/C G/A G/G T/T C/C G/A C/C C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089 15093
Sand small to the Market court court of the Market court of the Ma	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/C C/C C/C	12/15 G/G G/G A/G C/C G/A G/C C/C C/C C/C C/C C/C C/C	G/G T/A C/C A/G G/C C/A T/T C/C G/G A/C C/C C/C	G/G G/G A/A C/C A/G G/C C/C C/C G/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G T/T C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

	HAPLO'	TYPE PA	TRa						PS ^b	PS
55	2/21	22/3		5 12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION°
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
-	G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
	C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
60	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	${ t T}/{ t T}$	T/T	T/T	9	12397
65	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
70	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	C/C ·	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
2000 2000 2000 2000 2000 2000 2000 200	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
Transport F. E. E.	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
1 626			3						h	
75		TYPE PA		0.406	00/11	10/5	00/0	00/10	PS ^b	PS
75	3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION°
	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION° 3102 3409
	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
50	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
50	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
50	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
50	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
5 0	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/C G/A G/C C/C G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/G A/A C/C G/A G/C G/C C/C G/G C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/C G/A G/C C/C G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/A C/C G/A C/C G/C G/C C/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
90	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G T/G A/A C/C A/G G/C G/C T/T C/C G/G A/A C/C T/T	G/G G/G A/A C/C G/A G/C G/G T/C C/C G/G C/C T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C T/T G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C G/G	2/16 G/G G/G A/A G/C C/C G/G T/T C/C G/G A/A C/C C/T G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C T/T G/G	G/G G/G A/A C/C G/A G/C G/C G/C C/C G/G C/C T/T G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C T/T G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932

	HAPLO'	TYPE PA	AIR ^a				PS ^b	PS
	22/12		12/3	12/2	14/6	16/4	NUMBER	POSITIONC
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	T/G	G/G	G/G	G/G	G/G	G/G	2	3409
100	A/A	A/A	A/A	A/A	A/A	G/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	C/C	C/C	T/C	C/C	7 .	11998
105	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	C/C	C/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
110	A/G		G/A	G/A	G/G	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/T	15	15093
	T/T	T/C	\mathtt{T}/\mathtt{T}	T/C	T/C	T/C	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
115	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
1 15 	_				a act		and 1 1	*.4 44 4
, 525 E. T. Z	a	Haplotype	pairs ar	e represe	nted as 1"	haplotyp	e/2" haploty	ype; with allele
elêne jez					rphism/2	polymo	rphism in ea	ach column;
U		PS = poly			rO. 1			
120	Ĭ.	Position o	1 PS in S	EQ ID N	O:1.			
	10. Th	e method	of claim	9, where	in the ide	ntified ge	notype of th	e individual co
	nu	cleotide p	air at eac	ch of PS1	-PS18, w	hich have	the position	and alternativ
	SE	Q ID NO	:1.					
	11. A	method fo	r identif	ying an a	ssociation	between	a trait and a	t least one hap
<u>r5</u>	pa	ir of the tu	ımor nec	rosis fact	tor recepto	or superfa	mily, memb	er 1A (TNFRS
ļ.	co	mprises c	omparing	g the freq	uency of	the haplot	ype or haplo	otype pair in a

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column; ^bPS = polymorphic site;

- The method of claim 9, wherein the identified genotype of the individual comprises the 10. nucleotide pair at each of PS1-PS18, which have the position and alternative alleles shown in SEQ ID NO:1.
- A method for identifying an association between a trait and at least one haplotype or haplotype 11. pair of the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-27 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

				HA]	PLO:	ГҮРЕ	NU	JMB1	ΣR ^a]	⊋S ^b	PS	
	1	2	3	4	5	6	7	8	9	10	NUME	ER	POS:	ITION°
	G	G	G	G	G	G	G	G	G	G		1	3102	
15	G	G	G	G	G	G	G	G	G	G		2	. 3409	
	A	Α	A	Α	A	Α	Α	A	Α	A	;	3	3438	
	С	С	С	C	C	С	С	С	С	С		4	3603	
	A	Α	A	A	A	A	A	G	G	G		5	405	
	G	G	G	G	G	G	G	G	G	G		6	4082	
20	С	С	С	С	C	С	С	С	С	С		7	119	
	G	G	G	G	G	G	G	A	G	G		3	123	
	${f T}$	Т	\mathbf{T}	\mathbf{T}	\mathbf{T}	T	\mathbf{T}	\mathbf{T}	С	${f T}$		9	123	
	С	С	С	C	С	С	С	С	С	C		10	124	
	C	С	С	C	С	С	С	С	С	С		11	126	
25	A	G	G	G	G	G	G	G	G	G		12	148	
	A	A	A	Α	A	G	G	G	A	A		13	149	
	С	C	С	С	\mathbf{T}	С	C	С	С	C		14	150	
	С	С	С	T	С	С	С	С	С	C		15	150	
	С	С	T	С	С	С	Τ	Τ	Т	C		16	155	
30	G	G	G	G	G	G	G	G	G	G		17	159	
. 48%	G	G	G	G	G	G	G	G	G	G		18	161	63
22.5														
166) 166)				T.T.7\	ים זכו	די ע ה ד	וד אי	TIME	гъa				pgb	Dς
inin Film Film Film Film Film Film Film Film	11	1	2			TYPE		UMB		1 Ω	10	20	PS ^b	PS POSITION ^C
	11		2	13	14	1	5	16	17	18 G	19 G	20 G	NUMBER	POSITIONC
The state of the s	G	G	;	13 G	14 G	1 G	5	16 G	17 G	G	G	G	NUMBER 1	POSITION ^c 3102
	G G	G	,	13 G G	14 G G	1 G G	5	16 G G	17 G G	G T	G T	G T	NUMBER 1 2	POSITION° 3102 3409
	G G A	G A	; ;	13 G G A	14 G G A	1 G G G	5	16 G G G	17 G G G	G T A	G T A	G T A	NUMBER 1 2 3	POSITION° 3102 3409 3438
III R	G G A C	G A C	; ;	13 G G A	14 G G A C	1 G G G C	5	16 G G G C	17 G G G C	G T A C	G T	G T A C	NUMBER 1 2 3 4	POSITION° 3102 3409
III R	G G A C G	G A C G		13 G G A C	14 G G A C G	1 G G C A	5	16 G G G	17 G G G	G T A	G T A C	G T A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438 3603
III R	G A C G	G A C G		13 G G A	14 G G A C	1 G G G C	5	16 G G G C A	17 G G C A	G T A C A	G T A C A	G T A C A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
	G G A C G	G A C G		13 G G A C G	14 G A C G	1 G G C A G	5	16 G G G C A G	17 G G C A G	G T A C A	G T A C A G	G T A C A G	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054 4082
agene groot group Nat (1977)	G A C G C	G A C G C		13 G G A C G G	14 G A C G G	1 G G C A G	5	16 G G C A G	17 G G C A G	G T A C A A	G T A C A G	G T A C A G C G T	NUMBER 1 2 3 4 5 6 7	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397
	G G C G C G	G G A G G		13 G G A C G G G	14 G G A C G G T	1 G G C A G C	5	16 G G C A G C	17 G G C A G T	G T A C A C G	G T A C A G C G	G T A C A G C G T C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
agene groot group Nat (1977)	G A C G G C G T	G A C G C C		13 G G A C G G C G T	14 G G A C G G T	1 GGGCA GGG	5	16 G G C A G C T	17 GGGCAGTGTCC	G T A C A C G T C	G T A C A G C G T	G T A C A G C G T C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	G A C G G C G T C	G A C G G C T		13 G G A C G G C G T C	14 G A C G G T C	1 G G C A G C G T C	5	16 G G C A G C G T C	17 GGGCAGTGTCCG	G T A C A C G T C T G	G T A C A G C G T C	G T A C A G C G T C C G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
	G G A C G G C G T C C G A	G G G G C C		13 GGACGGCGTCTGA	14 G A C G G T C C G G	1 G G C C C C C C A	5	16 GGCAGCGTCC	17 GGGCAGTGTCCGA	G T A C A A C G T C T G A	G T A C A G C G T C C G A	G T A C A G C G T C C G G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
	G G A C G G C G T C C G A C	G G G G G G G G G G		13 GGACGGCGTCTGAC	14 G A C G G T C C G G C	1 G G G C A G C G T C C G A C	5	16 G G C A G C G T C C G A C	17 GGGCAGTGTCCGAC	G T A C A A C G T C T G A C	G T A C A G C G T C C G A C	G T A C A G C G T C C G G C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
	G G A C G G C G T C C G A C C	G G G G G G G G G G G G G G G G G G G		13 GGACGGCGTCTGACC	14 G A C G G T C C G G C C	1 G G G C A G C G T C C G A C C	5	16 GGGCAGCGTCCGACC	17 GGGCAGTGTCCGACC	G T A C A A C G T C T G A C C	G T A C A G C G T C C G A C C	G T A C A G C G T C C G G C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	G G A C G G C G T C C G A C C T	G G G G G G G G G G G G G G G G G G G		13 GGACGGCGTCTGACCT	14 G G A C G G T G T C C G G C C T	1 G G G C A G C G G A C C C	5	16 G G C C G T C C G A C C T	17 GGGCAGTGTCCGACCC	G T A C A A C G T C T G A C C T	G T A C A G C G T C C G A C C T	G T A C A G C G T C C G G C C T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
	G G A C G G C G T C C G A C C	G G G G G G G G G G G G G G G G G G G		13 GGACGGCGTCTGACC	14 G A C G G T C C G G C C	1 G G G C A G C G T C C G A C C	5	16 GGGCAGCGTCCGACC	17 GGGCAGTGTCCGACC	G T A C A A C G T C T G A C C	G T A C A G C G T C C G A C C	G T A C A G C G T C C G G C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

			HA.	PLOT	YPE	NUMB:	ERª	P	S ^b	PS
55	21	22	23	24	25	26	27	N.	UMBER	POSITION°
	G	G	G	G	G	G	\mathbf{T}	1		3102
	\mathbf{T}	${f T}$	T	T	\mathbf{T}	\mathbf{T}	G	2		3409
	A	Α.	A	A	A	G	G	3		3438
	С	Ċ	C	С	G	С	C	4		3603
60	A	A	A	G	A	A	A	5		4054
	G	G	G	G	G	G	G	6		4082
	С	С	С	С	С	С	C	7		11998
	G	G	G	G	G	G	G	8		12356
	T	T	${f T}$	T	${f T}$	\mathbf{T}	\mathbf{T}	9		12397
65	C	С	T	С	С	С	С	1	0	12489
	\mathbf{T}	\mathbf{T}	\mathbf{T}	T	${f T}$	С	C	1	1	12653
	G	G	G	G	G	G	G	1:	2	14824
	A	A	A	A	A	A	А	1	3	14990
	С	С	C	С	С	С	С	1	4	15089
70	С	С	С	С	C	С	С	1	5	15093
	С	T	${f T}$	${f T}$	${f T}$	С	${f T}$	1	6	15529
	G	G	G	G	G	G	G	1	7	15932
street.	G	G	G	G	G	G	A	1	8	16165
STATE Email Email		3 4 11	1 0		1 .			1 7 7 / 2 / 2 / 2	1 1	

^aAlleles for haplotypes are presented 5' to 3' in each column;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

	HAPLOI	TYPE PA	IR ^a						PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	$POSITION^c$
85	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2 .	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
90	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
, ,	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
95	C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	c/c	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
100	T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
Security Sec	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
LEE	-, -	-, -	-, -	•						
2007 2. 2. 3 4400000	HAPLO:	TYPE PA	IR ^a						PS ^b	PS
105		TYPE PA	IR ^a 12/1	5 22/8	2/9	3/21	2/15	12/17	PS ^b NUMBER	POSITIONC
105	HAPLOT 2/19 G/G	TYPE PA 3/14 G/G	IR ^a 12/1! G/G	5 22/8 G/G	2/9 G/G	3/21 G/G	2/15 G/G	12/17 G/G	NUMBER 1	POSITION° 3102
105	2/19	3/14	12/1		•				NUMBER 1 2	POSITION ^c 3102 3409
105	2/19 G/G	3/14 G/G	12/19 G/G	G/G	G/G	G/G	G/G G/G A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION° 3102 3409 3438
105	2/19 G/G G/T	3/14 G/G G/G	12/1! G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
tues pues quess	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/1! G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
1 LO	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/15 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
1 LO	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/19 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
110	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/19 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T	12/15 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
110 110 115	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
110 110 115	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/19 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
110 110 115	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/19 G/G G/G A/G C/C G/A G/G C/C G/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
110 110 115	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C	12/19 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
110 110 115	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G	12/19 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C G/G A/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T C/C G/G G/A C/C G/G G/A C/C G/C G/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G A/C C/C T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C T/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/C C/C G/C C/C C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

125	HAPLO	TYPE PA	IRa						PS ^b	PS
	2/21	22/3		512/25	12/24	12/13	3/16	22/16	NUMBER	POSITIONC
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
	A/A	A/A	A/A		A/A	A/A	A/G	A/G	3	3438
130	C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	g/G	6	4082
	C/C	.C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
135	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	c/c	10	12489
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
140	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
1.0	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
1 4-5	0, 0	0,0	-, -	-, -	-, -	-, -	-, -	-, -		
140										
143	HAPLO	TYPE PA	IR ^a						PS ^b	PS
143		TYPE PA 22/10		2/26	22/11	12/7	22/2	22/18		PS POSITION ^c
143	3/27	22/10	2/16	2/26 G/G	22/11 G/G	12/7 G/G	22/2 G/G	22/18 G/G	NUMBER	${\tt POSITION}^{\tt c}$
	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION° 3102 3409
150	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	G/G T/G A/A	G/G T/T A/A	NUMBER 1	POSITION ^c 3102 3409 3438
150	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
1 500	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438
	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603 4054
	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082
150 mg	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
1 The second sec	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
1 500	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
1 The second sec	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
1 To the state of	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C	2/16 G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
1 500	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
1 To the state of	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G G/G A/A C/C G/A G/C C/C G/G G/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
1 To the state of	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/C C/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C C/C	G/G G/A C/C G/A G/C G/C G/C G/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
1 To the state of	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/A C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/A C/C T/T	G/G G/G A/A C/C G/A G/C G/C G/C C/C G/C C/C T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
1 To the state of	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/C C/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C C/C	G/G G/A C/C G/A G/C G/C G/C G/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

	HAPLOT	YPE PA	IR ^a				PS ^b	PS
	22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION°
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
170	T/G	G/G	G/G	G/G	G/G	G/G	2	3409
	A/A	A/A	A/A	A/A	A/A	G/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
175	C/C	C/C	C/C	C/C	T/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	C/C	C/C	11	12653
180	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/G	G/A	G/A	G/A	G/G	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/T	15	15093
	T/T	T/C	T/T	T/C	T/C	T/C	16	15529
185	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

- 12. The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF1A.
- 13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF1A gene at a region containing the polymorphic site.
- 15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-10, the complements of SEQ ID NOS:4-10, and SEQ ID NOS:11-24.
- 16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.
- 17. The primer-extension oligonucleotide of claim 16, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:25-38.
- 18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS4, PS12, PS14, PS15, PS17 and

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

- PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 19. The kit of claim 18, which further comprises oligonucleotides designed to genotype each of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, having the location and alternative alleles shown in SEQ ID NO:1.
- 20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the TNFRSF1A isogene is selected from the group consisting of isogenes 1-27 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

											1		
		I	SOG	ENE	NU	MBE	R^a			PS ^b	R _S	SEQ ID	REGION
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION°	NO.	EXAMINED ^d
G	G	G	G	G	G	G	G	G	G	1	31\02	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	34 0 ,9	1	2920-4210
A	Α	A	A	Α	A	A	А	A	A	3	3438	1	2920-4210
С	C	С	С	С	С	C	C	С	С	4	3603∖	1	2920-4210
A.	A	А	A	Α	Α	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082 \	1	2920-4210
С	С	С	С	С	С	С	С	С	С	7	11998 \	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	\mathbf{T}	\mathbf{T}	\mathbf{T}	${f T}$	T	T	\mathbf{T}	С	\mathbf{T}	9	12397	1	11417-12926
С	С	С	C	С	С	С	C	С	С	10	12489	\ 1	11417-12926
С	С	С	С	С	С	С	С	С	С	11	12653	A	11417-12926
Α	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	Α	Α	Α	G	G	G	Α	A	13	14990	1	14634-16768
С	С	С	С	T	С	С	С	С	С	14	15089	1	14634-16768
С	С	С	\mathbf{T}	С	С	C	С	С	C	15	15093	1	14634-16768
С	С	T	С	С	С	\mathbf{T}	\mathbf{T}	${ m T}$	С	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768
												Y	A

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			•	NUMI	3ER ^a					PS^b	PS	SEQ		REGION
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITI		NO.	EXAMINED ^d
G	G	G	G \	G	G	G	G	G	G	1	3102	1		920-4210
G	G	G	G	∖ G	G	G	${ m T}$	${f T}$	${f T}$	2	3409	1	2	920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2:	920-4210
С	С	C	C	9	С	С	С	С	С	4	3603	1	25	920-4210
G	G	G	G	A\	A	A	A	A	A	5	4054	1	25	920-4210
G	G	G	G	G \	G	G	A	G	G	6	4082	1	2	920-4210
С	С	С	\mathbf{T}	C	\ C	\mathbf{T}	С	С	С	7	11998	1	1:	1417-12926
G	G	G	G	G	Æ	G	G	G	G	8	12356	1		1417-12926
T	T	${f T}$	\mathbf{T}	\mathbf{T}	$\sqrt{\Gamma}$	\mathbf{T}	\mathbf{T}	T	T	9	12397	1	1:	1417-12926
С	С	С	С	С	c/	С	C	C	С	10	12489	1	1:	1417-12926
C	С	T	С	С	c \	C	\mathbf{T}	С	С	11	12653	1	1:	1417-12926
G	G	G	G	G	G	\G	G	G .	G	12	14824	1	1	4634-16768
А	G	A	G	A	A	$^{/\!\!\!\!/}$	A	A	G	13	14990	1	1	4634-16768
С	С	С	С	С	С	9	С	С	С	14	15089	1	1	4634-16768
С	C	C	С	C	C	c\	C	С	С	15	15093	1	1	4634-16768
T	${f T}$	Т	${f T}$	С	\mathbf{T}	C)	T	T	${f T}$	16	15529	1	1	4634-16768
G	G	G	G	G	G	G	\ G	A	G	17	15932	1	1	4634-16768
G	G	G	G	G	· G	G	Ġ	G	G	18	16165	1	1	4634-16768
							1							
		ISO	SENE	NUME	3ERª		₽ / Ş	р		PS	SEQ ID	REG	ION	
21	22	23	24	25	26	27	NUM	BER		POSITIONC	NO.	EXA	MINE	D ^d
G	G	G	G	G	G	\mathbf{T}		1		3102	1	292	0-42	10
\mathbf{T}	${f T}$	${\mathbb T}$	\mathbf{T}	\mathbf{T}	${f T}$	G		\2		3409	1	292	0 - 42	10
A	A	A								0 - 0 5		202	0 42	
С		T7	A	\boldsymbol{A}	G	G		Ĕ		3438	1 .		0-42	1.0
\sim	С	C	A C	A G	G C	G C		4			1 1	292		
A	C A				-	_				3438		292 292 292	0-42 0-42 0-42	10 10
	-	C	С	G	C	C		4		3438 3603	1	292 292 292	0-42	10 10
A	A	C A	C G	G A	C A	C A		4 \ 5		3438 3603 4054	1 1	292 292 292 292	0-42 0-42 0-42	10 10 10
A G	A G	C A G	C G G	G A G	C A G	C A G		4 \ 5 6		3438 3603 4054 4082	1 1 1	292 292 292 292 114	0-42 0-42 0-42 0-42	10 10 10 2926
A G C	A G C	C A G C	C G G C	G A G C	C A G C	C A G C		4 \ 5 6 7		3438 3603 4054 4082 11998	1 1 1 1	292 292 292 292 114 114	0-42 0-42 0-42 0-42 17-1	10 10 10 2926 2926
A G C G	A G C G	C A G C G	C G G C G	G A G C	C A G C	C A G C G		4 \ 5 6 7 8		3438 3603 4054 4082 11998 12356	1 1 1 1 1	292 292 292 292 114 114	0-42 0-42 0-42 0-42 17-1:	10 10 10 2926 2926 2926
A G C G	A G C G	C A G C G	C G G C G	G A G C G	C A G C G	C A G C G T		4 \ 5 6 7 8 9		3438 3603 4054 4082 11998 12356 12397	1 1 1 1 1	292 292 292 292 114 114 114	0-42 0-42 0-42 0-42 17-1: 17-1:	10 10 10 2926 2926 2926 2926
A G C G T	A G C G T C	C A G C G T	C G G C G T C	G A G C G T	C A G C G T	C A G C G T C		4 \ 5 6 7 8 9 10		3438 3603 4054 4082 11998 12356 12397 12489	1 1 1 1 1 1	292 292 292 292 114 114 114 114	0-42 0-42 0-42 0-42 17-1: 17-1: 17-1:	10 10 10 2926 2926 2926 2926 2926
A G C G T C	A G C G T C	C A G C G T T	C G G C G T C	G A G C G T C	C A G C G T C C	C A G C G T C C		4\ 5 6 7 8 9 10		3438 3603 4054 4082 11998 12356 12397 12489 2653	1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 114	0-42 0-42 0-42 0-42 17-1: 17-1: 17-1: 17-1:	10 10 10 2926 2926 2926 2926 2926 2926
A G C G T C	A G C G T C T G	C A G C G T T	C G G C G T C T G	G A G C G T C	C A G C G T C G	C A G C G T C G		4\ 5 6 7 8 9 10 11		3438 3603 4054 4082 11998 12356 12397 12489 12653 14824	1 1 1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 114 146 146	0-42 0-42 0-42 0-42 17-1: 17-1: 17-1: 17-1: 34-1	10 10 10 2926 2926 2926 2926 2926 6768
A G C G T C T G A	A G C G T C T G A	C A G C G T T G A	C G G C G T C T G A	G A G C G T C T G A	C A G C G T C G A	C A G C G T C C G A		4\ 5 6 7 8 9 10 11 12		3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990	1 1 1 1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 114 146 146	0-42 0-42 0-42 0-42 17-1: 17-1: 17-1: 17-1: 34-1 34-1	10 10 10 2926 2926 2926 2926 2926 6768 6768
A G C G T C T G A	A G C G T C T G A C	C A G C G T T G A C	C G G C G T C T G A	G A G C G T C T G A	C A G C G T C G A	C A G C G T C C G A C		4\ 5 6 7 8 9 10 11 12 13		3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089	1 1 1 1 1 1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 146 146 146	0-42 0-42 0-42 0-42 17-1 17-1 17-1 17-1 34-1 34-1	10 10 10 2926 2926 2926 2926 2926 6768 6768 6768
A G C G T C T G A C C	A G C G T C T G A C C	C A G C G T T G A C C	C G G C G T C T G A C C	G A G C G T C T G A C C	C A G C G T C C G A C C	C A G C G T C C G A C C		4\ 5 6 7 8 9 10 11 12 13 14		3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15083	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 146 146 146	0-42 0-42 0-42 17-1: 17-1: 17-1: 17-1: 34-1: 34-1: 34-1: 34-1:	10 10 10 2926 2926 2926 2926 2926 6768 6768 6768
A G C G T C T G A C C C	A G C G T C T G A C C	C A G C G T T T G A C C T	C G G C G T C T G A C C T	G A G C G T C T G A C C T	C A G C G T C C G A C C C	C A G C G T C C G A C C T		4\ 5 6 7 8 9 10 11 12 13 14 15		3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15083 15529	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	292 292 292 292 114 114 114 114 146 146 146 146	0-42 0-42 0-42 17-1: 17-1: 17-1: 17-1: 34-1: 34-1: 34-1: 34-1: 34-1:	10 10 10 2926 2926 2926 2926 2926 6768 6768 6768 6768

^aAlleles for isogenes are presented 5′ to 3′ in each column;

- (b) a second nucleotide sequence which is complementary to the first nucleotide sequence.
- 21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.
- 22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 20, wherein the organism expresses a TNFRSF1A protein that is encoded by the first nucleotide sequence.

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.

5

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the selected polymorphism has the position set forth in the table immediately below:

	_	_			ENE				_	\	PS		PS	SEQ ID	REGIO	
1.0	1	2	3	4	5	6	7	8	9	10	/NUMBI	ER	POSITION		EXAMI	
10	G	G	G	G	G	G	G	G	G	G	$\begin{pmatrix} 1 \\ 0 \end{pmatrix}$		3102	1	2920-	
	G	G	G	G	G	G	G	G	G	G	\ 2		3409	1	2920-	
	A	A	A.	A	A	A	A	A	A	A	\3		3438	1	2920-	
	С	С	C	C	C	С	С	С	С	С	\ \		3603	1	2920-	
1.5	A	A	A	A	A,	A	A	G	G	G	É		4054	1	2920- 2920-	
15	G	G	G	G	G	G	G	G	G	G	6/		4082	1		
in the second	С	С	С	С	С	С	C	С	С	С	7 '	1	11998	1 1		-12926 -12926
terni Litte	G	G	G	G	G	G	G	A	G	G	8 9		12356 12397	1		-12926 -12926
	T	T C	T C	T	T	T C	T C	T C	C C	T C	9 10	\	12397	1		-12926
*## ***	С	C	C	C C	C C	C	C	C	C	C	11	1	12489	1		-12926
20	C	G	G	G	G	G	G	G	G	G	12	\	14824	1		-16768
LF	A	A	A		A	G	G	G	A	A	13	,	14990	1		-16768
1,171	A C	C	C	A C	A T	C	C	C	C	A C	13		15089	1		-16768
101812 2 2 101812	C	C	C	T	C	С	C	C	C	C	15		15093	1		-16768
25	C	C	T	C	С	С	T	T	T	C	16		15529	1		-16768
<i>23</i>	G	G	G	G	G	G	G	G	G	G	17		15,932	1		-16768
2000) 1 1 1988)	G	G	G	G G	G	G	G	G	G	G	18		16165	1		-16768
Ü	G	G	· .	G	G	G	G	G	G	Ģ	10		10103	_	T-00-	10,00
in he													1			
LLİ			Т:	SOG	ENE	NU	MBE	Ra					PS ^b \	PS	SEO I	D REGION
14) 30	11	12			ENE 14		MBE		1.7	18	1.9	20	PS ^b \ NUMBER	PS POSITI	SEQ I ON° NO	
30	11 G	12 G	2 1	L3	14	NUI 15 G	ō :	16	17 G	18 G	19 G	20 G	1	PS POSITI 3102		and the second s
30	G	G	2 1	L3 3		15	ā ā		_		19 G T		NUMBER 1	POSITI	ONc NO	O. EXAMINED ^d
30			2 1	L3 3	14 G	15 G	5 ((16 G	G	G	G	G	NUMBER	POSITION 3102 3409	ON° NO 1	D. EXAMINED ^d 2920-4210
30	G G	G G	2 1	3 3 4	14 G G	15 G G	ā : (16 G G	G G	G T	G T	G T	NUMBER 1 2	POSITION 3102 3409	ON° NO 1 1	D. EXAMINED ^d 2920-4210 2920-4210
30	G G A	G G A	2 1 ((13 3 4	14 G G A	15 G G G	ō :	16 G G	G G G	G T A	G T A	G T A	NUMBER 1 2 3	POSITI 3102 3409 3438	ON° NO 1 1 1	D. EXAMINED ^d 2920-4210 2920-4210 2920-4210
30	G G A C	G G A C	2 1 ((L3 S	14 G G A C	15 G G G C	5 . (((16 G G C	G G G C	G T A C	G T A C	G T A	NUMBER 1 2 3 4	POSITI 3102 3409 3438 3603	ON ^c NO 1 1 1 1	D. EXAMINED ^d 2920-4210 2920-4210 2920-4210 2920-4210
30	G G A C	G G A C G	2 1 ((([3	14 G G A C	15 G G G C A	5 (((((16 G G G C A	G G C A	G T A C	G T A C A	G T A C A	NUMBER 1 2 3 4 5	POSITION 3102 3409 3438 3603 4054	ON° NO 1 1 1 1 1	D. EXAMINED ^d 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926
30	G G A C G	G G A C G	2 1 (((((13 13 13	14 G G A C G G	15 G G C A G	() () () () () () () () () ()	16 G G C A	G G C A G	G T A C A	G T A C A G	G T A C A G	NUMBER 1 2 3 4 5	POSITION 3102 3409 3438 3603 4054 4082 11998 2356	ON° NO 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926
30	G G A C G G C	G G C G C	2 1 ((((((13 13 13 13 13 13 13 13 13 13 13 13 13 1	14 G G A C G G T	15 G G C A G C	Š : Š (16 G G G C A G C	G G C A G	G T A C A A	G T A C A G C G	G T A C A G	NUMBER 1 2 3 4 5 6 7 8	POSITION 3102 3409 3438 3603 4054 4082 11998 2356 12397	ON° NO 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926
30	G G A C G G C	G G A C G G C G	2 1 () () () () () ()	13 13 13 13 13 13 13 13 13 13 13 13 13 1	14 G G A C G T	15 G G C A G C G		16 G G C A G C G	G G C A G T	G T A C A C G	G T A C A G C G T C	G T A C A G C G	NUMBER 1 2 3 4 5 6 7	POSITION 3102 3409 3438 3603 4054 4082 11998 2356 12397 12489	ON° NO 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926
30	G G A C G G C G T	G G C G G C	2 1 () () () () () ()		14 G G A C G G T G	15 GGGCAGCGT	; č	16 G G C A G C G T	G G C A G T G T C C	G T A C A C G	G T A C A G C G T C C	G T A C A G C G T C C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926
30	G G A C G G C G T C	G G A C G G C G T C	2 1 C C C C C C		14 G G A C G G T G T C	15 GGGCAGCGTC		16 G G C A G C G F C	G G C A G T G T C	G T A C A C G T	G T A C A G C G T C	G T A C A G C G T C C G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926
30	G G A C G G C G T C C	GGACGGCGTCC	2 1 C C C C C C C		14 G G A C G G T G T C C	15 GGGCAGCGTCC		16 G G C A G C G T C C	G G C A G T G T C C	G T A C A C G T C T G A	G T A C A G C G T C G G A	G T A C A G C G T C C G G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12357 12489 12653 14824 14990	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 14634-16768
30 35 40	G G A C G G C G T C C G	GGACGGCGTCCG	2 1 C C C C C C C C		14 GGACGGTGTCCGGC	1. GGGCAGCGTCCG	5		G G G C A G T G T C C	G T A C A C G T C T	G T A C A G C G T C C G A C	G T A C A G C G T C C G G C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12357 12489 12653 14824 14990 15089	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 14634-16768 14634-16768
30	G G A C G G C G T C C G A C C	G G A C G G C G T C C G G C C			$\begin{array}{cccccccccccccccccccccccccccccccccccc$	15 G G G C A G C G T C C G A C C			G G G C A G T G T C C G A C C	G T A C A A C G T C T G A C C	G T A C A G C G T C C G A C C	G T A C A G C G T C C G G C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 14634-16768 14634-16768
30 35 40	GGACGGCGTCCGACCT	G G A C G G C G T C C G G C C T			14 G A C G G T G T C C G G C C T	15 G G G C A G C C C G A C C C			GGGCAGTGTCCGACCC	G T A C A A C G T C T G A C C T	G T A C A G C G T C C G A C C T	G T A C A G C G T C C G G C C T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITI 3102 3409 3438 3603 4054 4082 11998 2356 12356 12397 12489 12653 14824 14990 15089 15093 15529	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-16768 14634-16768 14634-16768
30 35 40	GGACGGCGTCCGACCTG	GGACGGCGTCCGGCCTG			$\begin{array}{cccccccccccccccccccccccccccccccccccc$	15 G G G C A G C G T C C G A C C C G			GGGCAGTGTCCGACCCG	G T A C A A C G T C T G A C C T G	G T A C A G C G T C C G A C C T A	G T A C A G C G T C C G G C C T G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITI 3102 3409 3438 3603 4054 4082 11998 2356 12356 12357 12489 12653 14824 14990 15089 15093 15529 15932	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 14634-16768 14634-16768 14634-16768
30 35 40	GGACGGCGTCCGACCT	G G A C G G C G T C C G G C C T			14 G A C G G T G T C C G G C C T	15 G G G C A G C C C G A C C C			GGGCAGTGTCCGACCC	G T A C A A C G T C T G A C C T	G T A C A G C G T C C G A C C T	G T A C A G C G T C C G G C C T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITI 3102 3409 3438 3603 4054 4082 11998 2356 12356 12397 12489 12653 14824 14990 15089 15093 15529	ON° NO 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-16768 14634-16768 14634-16768

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		ISOG	ENE	NUMB	€R ^a		PS ^b	PS	SEQ ID	REGION
21	22	23	24	25	\$ 6	27	NUMBER	POSITION°	NO.	EXAMINED ^d
G	G	G	G	G	Ì	T	1	3102	1	2920-4210
T	T	Т	T	\mathbf{T}	T	G	2	3409	1	2920-4210
A	A	A	A	A	G \	G	3	3438	1	2920-4210
С	С	С	С	G	c '	\ C	4	3603	1	2920-4210
A	A	A	G	A	A	\not	5	4054	1	2920-4210
G	G	G	G	G	G	ġ	6	4082	1	2920-4210
С	С	С	С	С	С	c/	7	11998	1	11417-12926
G	G	G	G	G	G	· G \	8	12356	1	11417-12926
\mathbf{T}	\mathbf{T}	${f T}$	T	Т	T	т '	9	12397	1	11417-12926
С	С	${f T}$	С	С	С	С	10	12489	1	11417-12926
\mathbf{T}	T	T	T	${f T}$	Ċ	С	\ 11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1 .	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
С	С	C '	С	С	С	С	14	15089	1	14634-16768
С	С	С	С	С	С	C	\ 15	15093	1	14634-16768
С	T	\mathbf{T}	\mathbf{T}	${ m T}$	С	T	\ 16	15529	1	14634-16768
G	G	G	G	G	G	G	1 7	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768
							\			

^aAlleles for isogenes are presented 5' to 3' in each column;

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and wherein each of the coding sequences comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isog	ene	Coding	Sequence	Number	PS	PS \
8	9	14,17	19		Number	Position
С	С	${f T}$	C		7	224
A	G	G	G·		8	362
${f T}$	С	${ m T}$	T		9	403
G	G	G	A		17	935

^aAlleles for the isogene coding sequence are presented 5′ to 3′ in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene;

- 26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein that is encoded by the polymorphic variant sequence.
- 27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.
- 28. An isolated fragment of a TNFRSF1A cDNA, wherein the fragment comprises adenine at a

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:2.

- position corresponding to nucleotide 935 in SEQ ID NO:2.
- An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises lysine at a position corresponding to amino acid position 312.
- 30. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.
- 31. A method for screening for drugs targeting the isolated polypeptide of claim 31 which comprises contacting the TNFRSF1A polymorphic variant with a candidate agent and assaying for binding activity.
- 32. An isolated fragment of the TNFRSF1A polypeptide, wherein the fragment comprises lysine at a position corresponding to amino acid position 312 in SEQ ID NO:3.
- A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 1A gene, comprising:
 - (a) a central processing unit (CPU);
 - (b) a communication interface;
 - (c) a display device;
 - (d) an input device; and
 - (e) a database containing the polymorphism data;

wherein the polymorphism data comprises any one or more of the haplotypes set forth in the table immediately below:

10				HA	PLO'	TYP:	E N	UMB1	ER		PS ^p	PS
Profit	1	2	3	4	5	6	7	8	9 `	10	NUMBER	POSITION°
	G	G	G	G	G	G	G	G	G	G	1	3102
	G	G	G	G	G	G	G	G	G	G `	_ 2	3409
	A	Α	Α	Α	A	Α	A	Α	A	A	3	3438
15	С	С	С	С	С	С	С	С	С	С	4	3603
	A	A	A	A	Α	A	Α	G	G	G	5	4054
	G	G	G	G	G	G	G	G	G	G	6	4082
	С	С	С	С	С	С	С	С	С	C	7	11998
	G	G	G	G	G	G	G	Α	G	G	8	12356
20	Т	${f T}$	${f T}$	${\mathbb T}$	\mathbf{T}	${f T}$	${f T}$	\mathbf{T}	С	T	9	12397
	С	С	С	С	С	С	С	С	С	С	10	12489
	С	C	\mathbb{C}_{+}	С	С	С	С	С	С	C	11	12653
	A	G	G	G	G	G	G	G	G	G	12	14824
	A	A	Α	Α	Α	G	G	G	Α	Α	13	14990
25	С	С	С	С	${f T}$	С	С	С	С	С	14	15089
	С	С	С	${f T}$	С	С	С	С	С	С	15	15093
	С	С	T	С	С	С	${f T}$	${ m T}$	T	С	16	15529
	G	G	G	G	G	G	G	G	G	G	17	15932
	G	G	G	G	G	G	G	G	G	G	18	16165
20												

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30														
			HA	PLOT	YPE :	NUMB	ER ^a					$\mathtt{PS}^\mathtt{b}$	PS	
	11	12	13	14	15	16	17	18	19	20	NU	MBER	${ t POSITION}^{ t c}$	
	G `	G	G	G	G	G	G	G	G	G		1	3102	
	G	Ġ\	G	G	G	G	G	\mathbf{T}	T	${f T}$		2	. 3409	
35	A	A	\ A	A	G	G	G	A	A	A		3	3438	
	С	С	Z	С	С	С	С	С	С	С		4	3603	
	G	G	G\	G	A	A	A	A	A	A		5	4054	
	G	G	G `	∖G	G	G	G	A	G	G		6	4082	
	Ċ	С	С	R	С	С	T	С	С	С		7	11998	
40	G	G	G	G	G	G	G	G	G	G		8	12356	
	T	Т	\mathbf{T}	\mathbf{T}	T	\mathbf{T}	\mathbf{T}	T	\mathbf{T}	T		9	12397	
	С	С	С	С	9	С	С	С	С	С		10	12489	
	С	С	\mathbf{T}	С	C \	∖ C	С	Т	С	С		11	12653	
	G	G	G	G	G	Ğ	G	G	G	G		12	14824	
45	A	G	A	G	A	A	A	A	A	G		13	14990	
	С	С	С	C	С	C `	\c	С	С	С		14	15089	
	C	C	C	C	С	С	Ġ	С	С	С		15	15093	
	${f T}$	Т	Т	Т	С	T	C /	Т	T	${f T}$		16	15529	
Market.	G	G	G	G	G	G	G	G	A	G		17	15932	
50	G	G	G	G	G	G	G	Ġ	G	G		18	16165	
12005 1805								/						
			HA	PLOT	YPE	NUMB	ERa			PS ^b		PS		
erijas 1 dec	21	22	23	24	25	26	27		`	NUMBE	ER	POSI	TION°	
60 š	G	G	G	G	G	G	$^{-}$ T		/-	1		3102		
55	${f T}$	\mathbf{T}	T	\mathbf{T}	T	${f T}$	G			2\		3409	•	
logi Lili	A	Α	A	A	A	G	G			3 \		3438		
	С	С	С	C	G	С	C		4	$4 \setminus$		3603	;	
Same St	A	A	A	G	A	A	A			5		4054		
244 244	G	G	G	G	G	G	G			6		4082		
60	С	С	C	C	С	C	С			7	\	1199	8	
1948 1 s	G	G	G	G	G	G	G			8		1235		
	T	T	${ m T}$	${f T}$	${f T}$	T	${f T}$:	9		1239		
lasi Lai	С	С	${f T}$	С	С	C	C·			10		1248		
(T. 100)	${f T}$	\mathbf{T}	${f T}$	${f T}$	T	С	С			11		1265		
65	G	G	G	G	G	G	G			12		1482		
	A	A	A	A	A	Α	A			13		1499	00 \	
	С	С	С	С	С	С	C			14		1508	9	
	С	С	С	С	С	С	С			15		1509)3	
	С	${f T}$	${f T}$	${f T}$	${f T}$	С	${f T}$			16		1552	.9	
70	G	G	G	G	G	G	G			17		1593	32	
	G	G	G	G	G	G	A			18		1616	55 /	
		^a Al	leles f	or hap	lotype	s are	presen	ited 5'	to 3':	in eacl	n col	umn;		
		^b PS	= pol	ymorī	hic si	te;							\	\
		°Po	sition	of PS	in SE	Q ID I	NO:1;							
75						•	,							

the haplotype pairs set forth in the table immediately below:

1										
	HAPLOT	YPE PA	IR ^a						PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITIONC
80	∖G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	GXG	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	c/c	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
85	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
05	C/C	c/c	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	c/c	C/C	C/C	C/C	C/T	C/C	10	12489
90	C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
70	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	c/c	C/C	C/C	C/C	15	15093
95	T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
1000 1000 1000 1000 1000 1000 1000 100	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G	G/G G/G	G/G G/G	G/G G/G	18	16165
	G/ G	G/G	G/ G	G/G	G/ G	/g/ G	G/G	G/G	10	10100
119100										
ide.	н л от.∩п	VDF DA	тра			A			DGb	DQ
ide.		YPE PA		522/8	2/9	A 3/21	2/15	12/17	PS ^b	PS POSTTION ^C
1 <mark>0</mark> 0	2/19	3/14	12/15		2/9 G/G	3/21 G/G	2/15 G/G	12/17 G/G	NUMBER	${\tt POSITION}^{\tt c}$
100 T	2/19 G/G	3/14 G/G	12/15 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION ^c 3102
100 U	2/19 G/G G/T	3/14 G/G G/G	12/15 G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITION ^c 3102 3409
100 T	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/15 G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/15 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
100 105 105	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/15 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
100	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/15 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
100 mg mg mg mg mg mg mg mg mg mg mg mg mg	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/15 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
100	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/G G/G G/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
100 ms for my fine 105 ms for my	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
100 mg mg mg mg mg mg mg mg mg mg mg mg mg	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G G/T G/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
100 ms for my fine 105 ms for my	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/C C/A G/G G/T G/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
100 ms for my fine 105 ms for my	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G	G/G G/G A/C C/A C/T G/T C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
100 ms for my fine 105 ms for my	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/C G/A G/T G/T C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
100 grant pro line 105 grant pro	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/T C/C G/G T/T C/C G/G A/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/C C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/G G/C G/G G/T G/C G/A C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
100 ms for my fine 105 ms for my	2/19 G/G G/T A/A C/C A/A G/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G T/T C/C C/C G/G A/C C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G C/C C/C	G/G G/G A/A C/C A/G G/C C/C C/C C/C C/C C/C	G/G G/T A/A C/C A/A G/C G/G T/T C/T G/G A/A C/C C/C	G/G G/G A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G G/C G/G G/T C/C G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
100 grant pro line 105 grant pro	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/T T/T C/C G/G C/C T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/A C/C T/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/C C/C T/T	G/G G/G A/A C/C A/G G/C C/C G/G T/C C/C G/A C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/A C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/C G/A G/T G/T C/C G/A C/C T/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
100 grant pro line 105 grant pro	2/19 G/G A/A C/C A/A G/G C/C G/G T/T C/C G/A C/C C/T G/A	3/14 G/G G/G A/A C/C A/G G/T C/C G/G T/T C/C G/G C/C T/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G G/A C/C G/G G/A C/C G/G	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/C C/C T/T G/G	G/G G/G A/A C/C A/G G/C C/C G/G A/A C/C C/C G/G A/A C/C C/T G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/A C/C G/G A/A C/C G/G	G/G G/G A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C C/C	G/G G/G G/G G/T C/C G/A C/C G/A C/C G/C G/C G/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
100 grant pro line 105 grant pro	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/T T/T C/C G/G C/C T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/A C/C T/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/C C/C T/T	G/G G/G A/A C/C A/G G/C C/C G/G T/C C/C G/A C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/A C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/C G/A G/T G/T C/C G/A C/C T/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

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120	(HAPLO	TYPE PA	.IR ^a						PS ^b	PS
	2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	${ t POSITION}^{ t c}$
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	G/T \	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438.
125	C/C	cyc	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	cxç	c/c	C/C	C/C	C/C	c/c	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
130	T/T	T/T	T/T	TVT	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	c/g	C/C	C/C	C/C	C/C	10	12489
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
135	C/C	C/C	C/C	C/C	c/c	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	c/c	C/C	C/C	C/C	15	15093
	C/C	T/T	T/T	T/T	T/T	TXT	T/T	T/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
	G/G	G/G	G/G	G/G	G/G	G/G \	G/G	G/G	18	16165
140		·	- ,	,			À			
L.J	HA DT O	TT 7 TT 7 TT 7					/7		h	
e Service	TAPLO.	LABE BY	IR"						PS ^b	PS
	3/27	TYPE PA 22/10		2/26	22/11	12/7	22/2	22/18	PS" NUMBER	PS POSITION ^c
	3/27	22/10	2/16	2/26 G/G	22/11 G/G		22/2			
				2/26 G/G G/T	22/11 G/G T/G	12/7 G/G G/G	. /	22/18 G/G \T/T	NUMBER	POSITION ^c
145	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G T/G	G/G	22/2 G/G T/G	G/G	NUMBER 1	POSITION ^c 3102
145	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G	G/G G/G	22/2 G/G	G/G T/T	NUMBER 1 2	POSITION ^c 3102 3409
145	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	22/2 G/G T/G A/A	G/G T/T A/A C/C	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
The state of the s	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	22/2 G/G T/G A/A C/C	G/G T/T A/A	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
The state of the s	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	22/2 G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	22/2 G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	22/2 G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T AXA C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 7 8	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
The state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 7 8 9	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G T/T	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
The state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	G/G G/G A/A C/C G/G C/C G/G T/T C/C G/G G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/C G/G T/T C/C G/G A/A C/C	G/G G/T A/C A/C G/C G/C G/C G/C C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/G A/A C/C G/A G/C G/G T/C C/C G/G G/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/T A/A C/A G/A C/C G/G T/T C/T G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/C A/A G/C G/G T/T C/C G/A C/C	G/G G/T A/C A/A G/C G/T C/C G/A C/C C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C C/C	G/G G/A C/A C/A G/C G/T C/C G/C C/C C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/TA C/A C/A C/G T/C T/T G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
1 Tools with the state of the s	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/A G/C C/C G/G T/T C/C G/A C/C C/T	G/G G/T A/C A/C G/C G/T C/C G/A C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C T/T	G/G G/G A/A C/C G/A G/C G/G C/C G/G C/C G/G C/C T/T	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C C/C T/C	G/G T/T A/A C/A G/A G/C G/G T/T C/C T/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

	HAPLO	TYPE PA	IR ^a				PS ^b	PS
	22×12	12/5	12/3	12/2	14/6	16/4	NUMBER	${\tt POSITION}^{\tt c}$
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
165	T/G `	\ G/G	G/G	G/G	G/G	G/G	2	3409
	A/A	AXA	A/A	A/A	A/A .	G/A	3	3438
	C/C	c/c/	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	GΧG	G/G	G/G	G/G	6	4082
170	C/C	C/C	c/c	C/C	T/C	C/C	7	11998
	G/G	G/G	G/G	ઉ√G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	c/c \	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	J&\C	C/C	11	12653
175	G/G	G/G	G/G	G/G	G/S	G/G	12	14824
	A/G	G/A	G/A	G/A	G/G \	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	`&\C	14	15089
	C/C	C/C	C/C	C/C	C/C	C /T	15	15093
	T/T	T/C	T/T	T/C	T/C	T/C \	1 6	15529
180	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st Haplotype/2nd Haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column; ^cPosition of PS in SEQ ID NO:1;

and the frequency data in Tables 6 and 7.

185

34. A genome anthology for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises two or more TNFRSF1A isogenes selected from the group consisting of isogenes 1-27 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

			I	SOG	ENE	NU	MBE	:R ^a			PS ^b	PS	SEQ ID	REGION
	1	2	3	4	5	6	7	8	9	10	NUMBER	${\tt POSITION}^{\tt c}$	NO.	$EXAMINED^d$
10	G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
	G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
	A	Α	Α	A	A	A	A	Α	A	А	3	3438	1	2920-4210
	С	С	С	С	С	С	С	С	С	С	4	3603	1	2920-4210
	A	A	Α	А	Α	Α	A	G	G	G	5	4054	1	2920-4210
15	G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
	С	С	С	C	С	С	С	С	С	С	7	11998	1	11417-12926
	G	G	G.	G	G	G	G	A	G	G	8	12356	1	11417-12926
	Т	Т	\mathbf{T}	${ m T}$	${ m T}$	${f T}$	T	T	С	T	9	12397	1	11417-12926
	С	С	С	С	С	С	С	С	С	С	10	12489	1	11417-12926
20	С	С	С	С	С	С	С	С	С	С	11	12653	1	11417-12926
	Α	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
	Α	A	Α	A	Α	G	G	G	A	A	13	14990	1	14634-16768
	С	С	С	С	Т	С	С	С	С	С	14	15089	1	14634-16768
	С	С	С	\mathbf{T}	С	С	С	С	С	С	15	15093	1	14634-16768
25	С	С	\mathbf{T}	C	С	С	\mathbf{T}	\mathbf{T}	T	С	16	15529	1	14634-16768
	G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
	G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

30	11 G	12 G	13 G	14 G	NUME 15 G	16 G	17 G	18 G	19 G	20 G	PS ^b NUMBER 1	PS POSITIO 3102	1 2	2920-4210
35	G A C G G C G	G A C G C G	G A C G G C G	G A C G G T G	G G C A G C	G G C A G C	G G C A G T G	T A C A C G	T A C A G C	T A C A G C	2 3 4 5 6 7 8	3409 3438 3603 4054 4082 11998 12356	1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926
40	T C	T C C	T C T	T C C	T C C	T C C	T C C	T C T	T C C	T C	9 10 11	12397 12489 12653	1 1	L1417-12926 L1417-12926 L1417-12926
	C G	G	G	G	G	G	G	G	G	C G	12	14824	1 1	L4634-16768
	A C	G C	A C	G C	A C	A C	A C	A C	A C	G C	13 14	14990 15089		L4634-16768 L4634-16768
45	C.	C	C	C	C	C	C	C	C	C	15	15093		L4634-16768
75	T.	T	T	Т	C	T	C	T	T	T	16	15529		L4634-16768
	Ğ	Ğ	Ğ	Ğ	Ğ	G	G	G	Ā	G	17	15932		L4634-16768
	G	G	G	G	G	G	G	G	G	G	18	16165		14634-16768
	21 G T A	22 G T A	ISOG 23 G T A	24 G T A	NUME 25 G T A	26 G T G	27 T G G	PS NUM	S ^b IBER 1 2 3	*	PS POSITION ^c 3102 3409 3438		REGION EXAMINE 2920-42 2920-42 2920-42	210 210
65	A .G C G T C T G A C C C G G	A G C G T C T G A C C T G G	C A G C G T T G A C C T G G	C G G C G T C T G A C C T G G	G A G C G T C T G A C C T G G	C A G C G G A C C C G G	C A G C G T C C G A C C T G A		4 5 6 7 8 9 10 11 12 13 14 15 16		3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932 16165	1 1 1 1 1 1 1 1 1 1 1 1 1 1	2920-42 2920-42 11417-1 11417-1 11417-1 11417-1 14634-1 14634-1 14634-1 14634-1 14634-1	210 210 210 12926 12926 12926 12926 12926 16768 16768 16768

^aAlleles for isogenes are presented 5' to 3' in each column; ^bPS = polymorphic site; ^cPosition of PS in SEQ ID NO:1; ^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.